RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/053,753A
Source: IFW16
Date Processed by STIC: 1-21-05

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 01/21/2005
PATENT APPLICATION: **US/10/053,753A** TIME: 16:08:51

Input Set : **A:\SeqListing05031.3.txt**
Output Set: **N:\CRF4\01212005\J053753A.raw**

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Lau, Lester F.
(ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
(iii) NUMBER OF SEQUENCES: 21
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Howrey Simon Arnold & White LLP
(B) STREET: 321 North Clark Street, Suite 3400
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: United States of America
(F) ZIP: 60610
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/10/053,753A**
C--> **(B) FILING DATE: 22-Jan-2002**
(C) CLASSIFICATION:
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clough, David W.
(B) REGISTRATION NUMBER: 36,107
(C) REFERENCE/DOCKET NUMBER: 05031.0003.CNUS02
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 312/595-1408
(B) TELEFAX: 312/595-2250
(C) TELEX:
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 180..1316
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61 CGAGAGCGCC CCAGAGAAGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG      60
63 AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTCC GGGCGCATTT GATCCCGCTG     120
65 CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GCTCGCCCCG GTTCCTCCTG CGCGCCACA      179
67 ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC       227
68 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
69   1               5                  10                  15
71 CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC       275
72 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
73              20                  25                  30
75 CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC       323
76 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
77          35                  40                  45
79 GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC       371
80 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
81      50                  55                  60
83 AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC       419
84 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
85  65                  70                  75                  80
87 GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA       467
88 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
89                  85                  90                  95
91 GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC       515
92 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
93              100                 105                 110
95 TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG       563
96 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
97          115                 120                 125
99 GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC       611
100 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
101     130                 135                 140
103 TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG       659
104 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
105 145                 150                 155                 160
107 TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT       707
108 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
109                 165                 170                 175
111 GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT       755
112 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
113             180                 185                 190
115 GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC       803
116 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
117         195                 200                 205
119 TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC       851
120 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
121     210                 215                 220
123 CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC       899
124 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
125 225                 230                 235                 240
127 TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC       947
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128 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
129                 245                 250                 255
131 CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA       995
132 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
133             260                 265                 270
135 CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG      1043
136 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
137         275                 280                 285
139 AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC      1091
140 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
141     290                 295                 300
143 AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC      1139
144 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
145 305                 310                 315                 320
147 TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA      1187
148 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
149                 325                 330                 335
151 GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA      1235
152 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
153             340                 345                 350
155 TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC      1283
156 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
157         355                 360                 365
159 AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCCT    1336
160 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
161     370                 375
163 AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG    1396
165 AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAACTGCC AAGGGGCTGA    1456
167 TGTGGACGGA CAGCAGCGCA GCCG                                          1480
169 (2) INFORMATION FOR SEQ ID NO: 2:
171      (i) SEQUENCE CHARACTERISTICS:
172           (A) LENGTH: 379 amino acids
173           (B) TYPE: amino acid
174           (D) TOPOLOGY: linear
176      (ii) MOLECULE TYPE: protein
178      (ix) FEATURE:
179           (A) NAME/KEY: misc_feature
180           (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"
182      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
184 Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
185   1               5                  10                  15
187 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
188              20                  25                  30
190 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
191          35                  40                  45
193 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
194      50                  55                  60
196 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
197  65                  70                  75                  80
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199 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
200                  85                  90                  95
202 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
203             100                 105                 110
205 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
206         115                 120                 125
208 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
209     130                 135                 140
211 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
212 145                 150                 155                 160
214 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
215                 165                 170                 175
217 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
218             180                 185                 190
220 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
221         195                 200                 205
223 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
224     210                 215                 220
226 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
227 225                 230                 235                 240
229 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
230                 245                 250                 255
232 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
233             260                 265                 270
235 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
236         275                 280                 285
238 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
239     290                 295                 300
241 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
242 305                 310                 315                 320
244 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
245                 325                 330                 335
247 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
248             340                 345                 350
250 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
251         355                 360                 365
253 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
254     370                 375
256 (2) INFORMATION FOR SEQ ID NO: 3:
258      (i) SEQUENCE CHARACTERISTICS:
259           (A) LENGTH: 1418 base pairs
260           (B) TYPE: nucleic acid
261           (C) STRANDEDNESS: single
262           (D) TOPOLOGY: linear
264     (ii) MOLECULE TYPE: protein
266     (ix) FEATURE:
267           (A) NAME/KEY: CDS
268           (B) LOCATION: 124..1266
270     (ix) FEATURE:
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Input Set : **A:\SeqListing05031.3.txt**
Output Set: **N:\CRF4\01212005\J053753A.raw**

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271           (A) NAME/KEY: misc_feature
272           (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"
274     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
276 GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCGACCCC GCTGCGCACG GCCTGTCCGC      60
278 TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC     120
280 ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT       168
281     Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
282       1               5                  10                  15
284 CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC       216
285 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
286                 20                  25                  30
288 TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG       264
289 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
290             35                  40                  45
292 GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC       312
293 Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
294           50                  55                  60
296 TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC       360
297 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
298       65                  70                  75
300 TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA       408
301 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
302  80                  85                  90                  95
304 GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA       456
305 Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
306                 100                 105                 110
308 AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC       504
309 Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
310             115                 120                 125
312 GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG       552
313 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
314           130                 135                 140
316 GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG       600
317 Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu
318       145                 150                 155
320 GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG       648
321 Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln
322  160                 165                 170                 175
324 GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG       696
325 Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu
326                 180                 185                 190
328 TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG       744
329 Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu
330             195                 200                 205
332 AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT       792
333 Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro
334           210                 215                 220
336 TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC       840
337 Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys
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VERIFICATION SUMMARY DATE: 01/21/2005
PATENT APPLICATION: **US/10/053,753A** TIME: 16:08:52

Input Set : **A:\SeqListing05031.3.txt**
Output Set: **N:\CRF4\01212005\J053753A.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:886 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:907 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:928 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:949 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:970 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:1000 M:111 C: (47) String data converted to upper case,
L:1017 M:111 C: (47) String data converted to upper case,